

In the Claims:

Claims 1-131. (Cancelled)

Claim 132.(Currently Amended) A fusion protein comprising a boiling stable polypeptide fused to an additional polypeptide, said boiling stable protein having an amino acid sequence at least 65 % identical to SEQ ID NO:2 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2, said protein having at least one conserved amino acid sequence in at least one region corresponding to amino acids 9-11, 47-49 and/or 61-75, of SEQ ID NO:2, wherein said additional polypeptide is selected from the group consisting of an aggregating protein, a messenger protein, a messenger protein receptor protein, a protein of an agent of an infectious disease, a protein of an agent of a non-infectious disease, an interferon protein, an interferon receptor protein, a protein antigen, a growth factor protein, an enzyme protein and a heterologous protein of transformed cells. ~~An isolated boiling stable polypeptide having a chaperone-like activity.~~

Claim 133. (Currently Amended) The fusion protein of claim 132, wherein said boiling stable protein is at least at least 75 % identical to SEQ ID NO:2~~The polypeptide of claim 132, encoded by a polynucleotide having a sequence at least 60 % identical with SEQ ID NOs:1, 5, 6, 34, 39 or 40, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals 9.~~

Claim 134. (Currently Amended) The fusion protein of claim 132, wherein said boiling stable protein has an amino acid sequence at least 80 % identical to SEQ ID NO:2~~The polypeptide of claim 132, having a sequence at least 60 % homologous to SEQ ID NOs:2 or 35, as determined using the BestFit software of the Wisconsin~~

~~sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.~~

Claim 135. (Currently Amended) The fusion protein of claim 132, wherein said boiling stable protein has an amino acid sequence at least 85 % identical to SEQ ID NO:2~~The polypeptide of claim 132 which is natively an oligomer.~~

Claim 136. (Currently Amended) The fusion protein of claim 132, wherein said boiling stable protein has an amino acid sequence at least 95 % identical to SEQ ID NO:2~~The polypeptide of claim 132, wherein said chaperone-like activity includes heat stabilization of proteins.~~

Claim 137. (Currently Amended) The fusion protein of claim 132, wherein said boiling stable protein has an amino acid sequence as set forth in SEQ ID NO:2~~An isolated detergent stable polypeptide having a chaperone like activity.~~

Claim 138. (Currently Amended) The fusion protein of claim 132, wherein said aggregating protein is a beta amyloid~~The polypeptide of claim 137 encoded by a polynucleotide having a sequence at least 60 % identical with SEQ ID NOs:1, 5, 6, 34, 39 or 40, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals 9.~~

Claim 139. (Currently Amended) The fusion protein of claim 132, wherein said messenger protein is a cytokine~~The polypeptide of claim 137, having a sequence at least 60 % homologous to SEQ ID NOs:2 or 35, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.~~

Claim 140. (Currently Amended) The fusion protein of claim 132, wherein said messenger protein receptor protein is a cytokine receptor.~~The polypeptide of claim 137 which is natively an oligomer.~~

Claim 141. (Currently Amended) The fusion protein of claim 132, wherein said protein of agents of infectious disease is a bacterial exported protein from pneumococci or streptococci.~~The polypeptide of claim 137, wherein said chaperone-like activity includes heat stabilization of proteins.~~

Claim 142. (Currently Amended) The fusion protein of claim 132, wherein said protein of agents of infectious disease is a protein of hepatitis B and transmissible gastroenteritis.~~An isolated protease-resistant polypeptide having a chaperone-like activity.~~

Claim 143. (Currently Amended) The fusion protein of claim 132, wherein said protein of agents of infectious disease is a protein of protozoa and helminthes.~~The polypeptide of claim 142 encoded by a polynucleotide having a sequence at least 60 % identical with SEQ ID NOs:1, 5, 6, 34, 39 or 40, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.~~

Claim 144. (Currently Amended) The fusion protein of claim 132, wherein said protein of non-infectious diseases is an autologous tumor cell protein or epitope thereof.~~The polypeptide of claim 142, having a sequence at least 60 % homologous to SEQ ID NOs:2 or 35, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.~~

Claim 145. (Currently Amended) The fusion protein of claim 132, wherein said protein of non-infectious diseases, such as poorly antigenic autologous tumor cell proteins or any of their epitopes, interferons and their receptor proteins. The polypeptide of claim 142 which is natively an oligomer.

Claim 146. (Currently Amended) The fusion protein of claim 132, wherein said enzyme is selected from the group consisting of a glycosyl-hydrolase, a peroxidase, a transferase, a kinase, a phosphatase, a sulfatase, a ligase, a restriction enzyme, a reverse-transcriptase and a nucleic acid polymerase. The fusion protein of claim 171, wherein said boiling stable protein is at least at least 75 % identical to SEQ ID NO:2. The polypeptide of claim 142, wherein said chaperone-like activity includes heat-stabilization of proteins.

Claim 147. (Cancelled)

Claim 148. (Withdrawn) A fusion protein comprising a denaturant stable and/or protease resistant polypeptide having a chaperone-like activity fused to an additional polypeptide.

Claim 149. (Withdrawn) The fusion protein of claim 148, wherein said denaturant stable and/or protease resistant polypeptide having said chaperone-like activity is fused to said additional polypeptide via a peptide bond.

Claim 150. (Withdrawn) The fusion protein of claim 148, wherein said denaturant stable and/or protease resistant polypeptide having said chaperone-like activity is fused to said additional polypeptide via a cross-linker.

Claim 151. (Withdrawn) The fusion protein of claim 148, having an oligomeric form.

Claim 152. (Withdrawn) A pharmaceutical composition, comprising, as an active ingredient, a denaturant stable and/or protease resistant protein, said denaturant stable and/or protease resistant protein having a chaperone-like activity, and a pharmaceutically acceptable carrier.

Claim 153. (Withdrawn) The pharmaceutical composition of claim 151, wherein said pharmaceutical composition is packaged in a package and identified in print for use in a wound healing application.

Claim 154. (Withdrawn) The pharmaceutical composition of claim 152, wherein said pharmaceutical composition is packaged in a package and identified in print for use in a strengthening and/or grooming hair, nail or skin application.

Claims 155-170. (Cancelled)

Claim 171. (Currently Amended) The fusion protein of claim 132, wherein said protein antigens are selected from the group consisting of insulin, a gastrin, an opioid, calcitonin and a malarial blood-stage antigen. A fusion protein comprising the boiling stable polypeptide having a chaperone like activity of claim 132 fused to an additional polypeptide.

Claim 172. (Currently Amended) The fusion protein of claim 132, wherein said additional polypeptide is a CBD polypeptide. The fusion protein of claim 171, having an oligomeric form.

Claim 173-176. Canceled